

SEQUENCE LISTING

<110> Presnell, Scott R.

Kuestner, Rolf E.

Gao, Zeren

<120> Human Cytokine Receptor

<130> 00-49

<160> 13

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 2383

<212> DNA

<213> Homo sapiens

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<221> CDS

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Met Ala Pro Trp Leu Gln Leu Cys Ser
1 5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg 160
Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
10 15 20 25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg 208
Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
30 35 40

agg atg aaa gcg gct gcc cga ccc cgg ctt tgt gtt gct aat gag gga 256
Arg Met Lys Ala Ala Ala Arg Pro Arg Leu Cys Val Ala Asn Glu Gly
45 50 55

gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc ttc aaa 304

cat gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag			832
His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys			
235	240	245	
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa			880
Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln			
250	255	260	265
act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat			928
Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp			
270	275	280	
tat ata att gag ctg gtg gat gac act aac aca aca aga aaa gtg atg			976
Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met			
285	290	295	
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga			1024
His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg			
300	305	310	
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg			1072
Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr			
315	320	325	
ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca			1120
Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser			
330	335	340	345
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc			1168
His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu			
350	355	360	
cca aga gag agg ctc cgg ccg cgg aag gtc ttt ctc tgc tat tcc			1216
Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser			
365	370	375	
agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc gcc tac			1264
Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr			
380	385	390	
ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg tgg gaa			1312
Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu			
395	400	405	

gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag			1360
Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys			
410	415	420	425
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag			1408
Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys			
430	435	440	
tac ttt gtg gac aag aac tac aaa cac aaa gga ggt ggc cga ggc			1456
Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Arg Gly			
445	450	455	
tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa			1504
Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu			
460	465	470	
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt			1552
Lys Leu Arg Gln Ala Lys Gln Ser Ser Ala Ala Leu Ser Lys Phe			
475	480	485	
atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc ggt atc			1600
Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile			
490	495	500	505
cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc			1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu			
510	515	520	
tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag			1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln			
525	530	535	
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc			1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly			
540	545	550	
cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag			1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu			
555	560	565	
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cca			1840

Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro				
570	575	580	585	
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt				1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val				
590	595	600		
tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta				1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu				
605	610	615		
aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag				1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln				
620	625	630		
cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cg				2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro				
635	640	645		
gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa				2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys				
650	655	660	665	
gcc ggc agc ccc tcg gac atg ccg cg gac tca ggc atc tat gac tcg				2128
Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser				
670	675	680		
tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg				2176
Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser				
685	690	695		
acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct				2224
Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser				
700	705	710		
tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc				2272
Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu				
715	720	725		
tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac act gat				2320
Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp				
730	735	740	745	

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cttttagctg 2383

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 35 40 45
 Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn
 50 55 60
 Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr
 65 70 75 80
 Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn Ile Thr
 85 90 95
 Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile Leu Trp
 100 105 110
 Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg Val Ile
 115 120 125
 Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu Ile Leu
 130 135 140
 Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly Met Glu
 145 150 155 160
 Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys
 165 170 175
 Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe
 180 185 190
 Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu
 195 200 205
 Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His
 210 215 220
 Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe Gly
 225 230 235 240

Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro Phe
 245 250 255
 Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr Ser Cys
 260 265 270
 Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp
 275 280 285
 Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro Val
 290 295 300
 His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro
 305 310 315 320
 Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg
 325 330 335
 Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Ser
 340 345 350
 Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg Pro
 355 360 365
 Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn His
 370 375 380
 Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly
 385 390 395 400
 Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu
 405 410 415
 Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
 420 425 430
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
 435 440 445
 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Glu Leu Phe
 450 455 460
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
 465 470 475 480
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
 485 490 495
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
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 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
 515 520 525
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
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 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
 545 550 555 560
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
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Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
 580 585 590
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 595 600 605
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
 610 615 620
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
 625 630 635 640
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 645 650 655
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
 660 665 670
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
 675 680 685
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
 690 695 700
 Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu Glu Glu
 705 710 715 720
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<210> 3

<211> 2259

<212> DNA

<213> Artificial Sequence

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<221> misc_feature

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<223> n = A,T,C or G

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tggmgnatga argcngcngc nmgnccnmgn ytntgygtng cnaaygargg ngtnggnccn	180
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gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att aaa aac	170	175	180	640
Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn				
gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt gac ctg	190	195	200	688
Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu				
ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag cct ccg	205	210	215	736
Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg				
aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc ttc gac	220	225	230	784
Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser Phe Asp				
cac gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac tac aag	235	240	245	832
His Ala Pro His Asn Phe Gly Phe Arg Phe Tyr Leu His Tyr Lys				
ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag gag caa	250	255	260	880
Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln				
act aca gag atg acc agc tgc ctc ctt caa aat gtt tct cca ggg gat	270	275	280	928
Thr Thr Glu Met Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp				
tat ata att gag ctg gtg gat gac act aac aca aca aag gtg atg	285	290	295	976
Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met				
cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc atc aga	300	305	310	1024
His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg				
gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc gcg acg	315	320	325	1072
Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr				

ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata tat tca Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser 330 335 340 345	1120
cat tta gat gaa gag agc tct gag tct tcc aca tac act gca gca ctc His Leu Asp Glu Glu Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu 350 355 360	1168
cca aga gag agg ctc cgg cgg cgg aag gtc ttt ctc tgc tat tcc Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser 365 370 375	1216
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gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc cag aag Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys 410 415 420 425	1360
atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt atg aag Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys 430 435 440	1408
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tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att gcc gaa Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu 460 465 470	1504
aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc aag ttt Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe 475 480 485	1552
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Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile			
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cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct cag ctc			1648
Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu			
510	515	520	
tgt tcc cac ctg cac tcc cga gac cac ggc ctc cag gag ccg ggg cag			1696
Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln			
525	530	535	
cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag tca ggc			1744
His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly			
540	545	550	
cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att gac gag			1792
Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu			
555	560	565	
gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct cct cca			1840
Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro			
570	575	580	585
ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc ttg gtt			1888
Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val			
590	595	600	
tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc tgc cta			1936
Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu			
605	610	615	
aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac tcc cag			1984
Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln			
620	625	630	
cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc cggt cct			2032
His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro			
635	640	645	
gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg gtg aaa			2080
Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys			
650	655	660	665

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tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga ctc tcg Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser 685 690 695	2176
acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc tcc tct Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser 700 705 710	2224
tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag ctc ctc Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu 715 720 725	2272
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Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Met Lys Ala Ala Ala Arg 35 40 45	
Pro Arg Leu Cys Val Ala Asn Glu Gly Val Gly Pro Ala Ser Arg Asn 50 55 60	
Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr Thr Tyr 65 70 75 80	

Leu	Asn	Pro	Val	Gly	Lys	His	Val	Ile	Ala	Asp	Ala	Gln	Asn	Ile	Thr
				85					90					95	
Ile	Ser	Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile	Leu	Trp
				100				105					110		
Ser	Pro	Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly	Phe	Arg	Val	Ile
				115			120					125			
Leu	Glu	Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Cys	Gln	Gln	Leu	Ile	Leu
				130		135					140				
Lys	Asp	Pro	Lys	Gln	Leu	Asn	Ser	Ser	Phe	Lys	Arg	Thr	Gly	Met	Glu
				145		150				155				160	
Ser	Gln	Pro	Phe	Leu	Asn	Met	Lys	Phe	Glu	Thr	Asp	Tyr	Phe	Val	Lys
				165			170						175		
Val	Val	Pro	Phe	Pro	Ser	Ile	Lys	Asn	Glu	Ser	Asn	Tyr	His	Pro	Phe
				180			185						190		
Phe	Phe	Arg	Thr	Arg	Ala	Cys	Asp	Leu	Leu	Gln	Pro	Asp	Asn	Leu	
				195			200				205				
Ala	Cys	Lys	Pro	Phe	Trp	Lys	Pro	Arg	Asn	Leu	Asn	Ile	Ser	Gln	His
				210		215					220				
Gly	Ser	Asp	Met	Gln	Val	Ser	Phe	Asp	His	Ala	Pro	His	Asn	Phe	Gly
				225		230			235				240		
Phe	Arg	Phe	Phe	Tyr	Leu	His	Tyr	Lys	Leu	Lys	His	Glu	Gly	Pro	Phe
				245			250					255			
Lys	Arg	Lys	Thr	Cys	Lys	Gln	Glu	Gln	Thr	Thr	Glu	Met	Thr	Ser	Cys
				260			265					270			
Leu	Leu	Gln	Asn	Val	Ser	Pro	Gly	Asp	Tyr	Ile	Ile	Glu	Leu	Val	Asp
				275			280					285			
Asp	Thr	Asn	Thr	Thr	Arg	Lys	Val	Met	His	Tyr	Ala	Leu	Lys	Pro	Val
				290		295					300				
His	Ser	Pro	Trp	Ala	Gly	Pro	Ile	Arg	Ala	Val	Ala	Ile	Thr	Val	Pro
				305		310				315				320	
Leu	Val	Val	Ile	Ser	Ala	Phe	Ala	Thr	Leu	Phe	Thr	Val	Met	Cys	Arg
					325			330					335		
Lys	Lys	Gln	Gln	Glu	Asn	Ile	Tyr	Ser	His	Leu	Asp	Glu	Glu	Ser	Ser
				340			345					350			
Glu	Ser	Ser	Thr	Tyr	Thr	Ala	Ala	Leu	Pro	Arg	Glu	Arg	Leu	Arg	Pro
				355			360					365			
Arg	Pro	Lys	Val	Phe	Leu	Cys	Tyr	Ser	Ser	Lys	Asp	Gly	Gln	Asn	His
				370		375					380				
Met	Asn	Val	Val	Gln	Cys	Phe	Ala	Tyr	Phe	Leu	Gln	Asp	Phe	Cys	Gly
				385		390				395				400	
Cys	Glu	Val	Ala	Leu	Asp	Leu	Trp	Glu	Asp	Phe	Ser	Leu	Cys	Arg	Glu
					405			410					415		

Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe Ile
 420 425 430
 Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn
 435 440 445
 Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu Phe
 450 455 460
 Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln
 465 470 475 480
 Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp Tyr
 485 490 495
 Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys Tyr
 500 505 510
 Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser Arg
 515 520 525
 Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser Arg
 530 535 540
 Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile
 545 550 555 560
 Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys
 565 570 575
 Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro Val
 580 585 590
 Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys Lys
 595 600 605
 Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val Leu
 610 615 620
 Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly Gly
 625 630 635 640
 Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala Ala
 645 650 655
 Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp Met
 660 665 670
 Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu
 675 680 685
 Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr Ser
 690 695 700
 Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu Glu Glu
 705 710 715 720
 Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys Ala
 725 730 735
 Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Ala Ala Pro
 740 745 750

Leu

<210> 6
 <211> 2259
 <212> DNA
 <213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:5.

<221> misc_feature
 <222> (1)...(2259)
 <223> n = A,T,C or G

<400> 6

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tggmgnatga	argcngcngc	nmgnccnmgn	ytntgygtng	cnaaygargg	ngtnggnccn	180
gcnwsnmgna	aywsnggnyt	ntayaayath	acnttyaart	aygayaaytg	yacnacntay	240
ytnaayccng	tngnaarca	ygttnathgcn	gaygcncara	ayathacnat	hwsncartay	300
gcntgycayg	aycargtngc	ngtnacnath	ytntggwsnc	cngngcnyt	nggnathgar	360
ttyttnaarg	gnttymngnt	nathyngar	garytnaarw	sngarggnmg	ncartgycar	420
carytnathy	tnaargaycc	naarcarytn	aaywsnwsnt	tyaarmgnac	nggnatggar	480
wsncarccnt	tyytnaayat	gaarttygar	acngaytayt	tygttnaargt	ngtnccnnty	540
ccnwsnatha	araaygarws	naaytaycay	ccnttatty	tymgnacnmg	ngcntgygay	600
ytnytnytn	arccngayaa	yytngcntgy	aarcnntty	ggaarccnmg	naayytnaay	660
athwsncarc	ayggnwsnga	yatgcargtn	wsnttgyayc	aygcnccnca	yaayttyggn	720
ttymgnatty	tytaytnca	ytayaarytn	aarcaygarg	gnccnattyaa	rmgnaaraacn	780
tgyaarcarg	arcacnacn	ngaratgacn	wsnttgyytny	tncaraaygt	nwsnccnggn	840
gaytayatha	thgarytngt	ngaygayacn	aayacnacnm	gnaargtnat	gcaytaygn	900
ytnaarcng	tncaywsncc	ntggcnggn	ccnathmgng	cngtngcnat	hacngtnccn	960
ytnngtngtna	thwsngcntt	ygcnacnytn	ttyacngtna	tgtgymgnaa	raarcarcar	1020
garaayath	aywsncayyt	ngaygargar	wsnwsngarw	snwsnacnta	yacngcngcn	1080
ytnccnmng	armgnytnmg	nccnmgnccn	aargtnatty	tntgytayws	nwsnaargay	1140
ggncaraayc	ayatgaaygt	ngtncartgy	ttygcntayt	tytncarga	yttytgyggn	1200
tgygargtng	cnytngayyt	ntgggargay	ttywsnytnt	gymgngargg	ncarmngngar	1260
tgggttnathc	araarathca	ygarwsncar	ttyathathg	tngtngtgyws	naarggnatg	1320
aartayttyg	tngayaaraa	raaytayaar	cayaarggng	ngggnmgngg	nwsnggnaar	1380
ggngarytnt	tyyngtngc	ngtnwsngcn	athgcngara	arytnmgnc	rgcnaarcar	1440
wsnwsnwsng	cngcnytnws	naarttyath	gcngrntayt	tygatyayws	ntgygarggn	1500
gaygtncnccng	gnathytnga	yytnwsnacn	aartaymgn	tnatggayaa	yytnccncar	1560
ytnngtgywsnc	ayytnccayws	nmgngaycay	ggnytnccarg	arccnggnca	rcayacnmgn	1620

carggnwsnm gnmgnayta yttymgnwsn aarwsnggnm gnwsnytna ygtngcnath 1680
 tgyaayatgc aycarttyat hgaygargar ccngaytgg tygaraarca rtygtncn 1740
 ttcayccnc cnccnytnmg ntaymgngar ccngtnytna araarttyga ywsnggnyn 1800
 gtnytnaayg aygtnatgtg yaarcnggn ccngarwsng ayttytgyt naargtngar 1860
 gcngcngtny tnngngcnac ngnccngcn gaywsncarc aygarwsnca rcayggngn 1920
 ytngaycarg ayggngargc ngnccngcn ytngayggnw sngcngcnyt ncarrccnyt 1980
 ytnccayacng tnaargcngg nwsnccnwsn gayatgcnm gngaywsngg nathtaygay 2040
 wsnwsngtnc cnwsnwsnga rytnwsnytn ccnytnatgg arggnytnws nacngaycar 2100
 acngaracnw snwsnytnac ngarwsngtn wsnwsnwsnw snggnytnng ngargargar 2160
 ccnccngcny tnccnwsnaa rytnytnwsn wsnggnwsnt gyaargcnga yytnggntgy 2220
 mgnwsntaya cngaygaryt ncaygcngcn gcnccnyt 2259

<210> 7
 <211> 2341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
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Met Ala Pro Trp Leu Gln Leu Cys Ser

1 5

gtc ttc ttt acg gtc aac gcc tgc ctc aac ggc tcg cag ctg gct gtg 160
 Val Phe Phe Thr Val Asn Ala Cys Leu Asn Gly Ser Gln Leu Ala Val
 10 15 20 25

gcc gct ggc ggg tcc ggc cgc gcg cgg ggc gcc gac acc tgt ggc tgg 208
 Ala Ala Gly Gly Ser Gly Arg Ala Arg Gly Ala Asp Thr Cys Gly Trp
 30 35 40

agg gga gtg ggg cca gcc agc aga aac agt ggg ctg tac aac atc acc 256
 Arg Gly Val Gly Pro Ala Ser Arg Asn Ser Gly Leu Tyr Asn Ile Thr
 45 50 55

ttc aaa tat gac aat tgt acc acc tac ttg aat cca gtg ggg aag cat 304
 Phe Lys Tyr Asp Asn Cys Thr Thr Tyr Leu Asn Pro Val Gly Lys His
 60 65 70

gtg att gct gac gcc cag aat atc acc atc agc cag tat gct tgc cat			352
Val Ile Ala Asp Ala Gln Asn Ile Thr Ile Ser Gln Tyr Ala Cys His			
75	80	85	
gac caa gtg gca gtc acc att ctt tgg tcc cca ggg gcc ctc ggc atc			400
Asp Gln Val Ala Val Thr Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile			
90	95	100	105
gaa ttc ctg aaa gga ttt cgg gta ata ctg gag gag ctg aag tcg gag			448
Glu Phe Leu Lys Gly Phe Arg Val Ile Leu Glu Glu Leu Lys Ser Glu			
110	115	120	
gga aga cag tgc caa caa ctg att cta aag gat ccg aag cag ctc aac			496
Gly Arg Gln Cys Gln Gln Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn			
125	130	135	
agt agc ttc aaa aga act gga atg gaa tct caa cct ttc ctg aat atg			544
Ser Ser Phe Lys Arg Thr Gly Met Glu Ser Gln Pro Phe Leu Asn Met			
140	145	150	
aaa ttt gaa acg gat tat ttc gta aag gtt gtc cct ttt cct tcc att			592
Lys Phe Glu Thr Asp Tyr Phe Val Lys Val Val Pro Phe Pro Ser Ile			
155	160	165	
aaa aac gaa agc aat tac cac cct ttc ttc ttt aga acc cga gcc tgt			640
Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Arg Thr Arg Ala Cys			
170	175	180	185
gac ctg ttg tta cag ccg gac aat cta gct tgt aaa ccc ttc tgg aag			688
Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys			
190	195	200	
cct ccg aac ctg aac atc agc cag cat ggc tcg gac atg cag gtg tcc			736
Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser Asp Met Gln Val Ser			
205	210	215	
ttc gac cat gca ccg cac aac ttc ggc ttc cgt ttc tat ctt cac			784
Phe Asp His Ala Pro His Asn Phe Gly Phe Arg Phe Phe Tyr Leu His			
220	225	230	
tac aag ctc aag cac gaa gga cct ttc aag cga aag acc tgt aag cag			832
Tyr Lys Leu Lys His Glu Gly Pro Phe Lys Arg Lys Thr Cys Lys Gln			
235	240	245	

gag caa act aca gag acg acc agc tgc ctc ctt caa aat gtt tct cca	880
Glu Gln Thr Thr Glu Thr Thr Ser Cys Leu Leu Gln Asn Val Ser Pro	
250 255 260 265	
ggg gat tat ata att gag ctg gtg gat gac act aac aca aca aga aaa	928
Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Thr Asn Thr Thr Arg Lys	
270 275 280	
gtg atg cat tat gcc tta aag cca gtg cac tcc ccg tgg gcc ggg ccc	976
Val Met His Tyr Ala Leu Lys Pro Val His Ser Pro Trp Ala Gly Pro	
285 290 295	
atc aga gcc gtg gcc atc aca gtg cca ctg gta gtc ata tcg gca ttc	1024
Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val Val Ile Ser Ala Phe	
300 305 310	
gcg acg ctc ttc act gtg atg tgc cgc aag aag caa caa gaa aat ata	1072
Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys Gln Gln Glu Asn Ile	
315 320 325	
tat tca cat tta gat gaa gag agc tct gag tct tcc aca tac act gca	1120
Tyr Ser His Leu Asp Glu Glu Ser Ser Glu Ser Thr Tyr Thr Ala	
330 335 340 345	
gca ctc cca aga gag agg ctc cgg cgg cgg aag gtc ttt ctc tgc	1168
Ala Leu Pro Arg Glu Arg Leu Arg Pro Arg Pro Lys Val Phe Leu Cys	
350 355 360	
tat tcc agt aaa gat ggc cag aat cac atg aat gtc gtc cag tgt ttc	1216
Tyr Ser Ser Lys Asp Gly Gln Asn His Met Asn Val Val Gln Cys Phe	
365 370 375	
gcc tac ttc ctc cag gac ttc tgt ggc tgt gag gtg gct ctg gac ctg	1264
Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu Val Ala Leu Asp Leu	
380 385 390	
tgg gaa gac ttc agc ctc tgt aga gaa ggg cag aga gaa tgg gtc atc	1312
Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln Arg Glu Trp Val Ile	
395 400 405	
cag aag atc cac gag tcc cag ttc atc att gtg gtt tgt tcc aaa ggt	1360

Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val Val Cys Ser Lys Gly			
410	415	420	425
atg aag tac ttt gtg gac aag aag aac tac aaa cac aaa gga ggt ggc			1408
Met Lys Tyr Phe Val Asp Lys Lys Asn Tyr Lys His Lys Gly Gly Gly			
430	435	440	
cga ggc tcg ggg aaa gga gag ctc ttc ctg gtg gcg gtg tca gcc att			1456
Arg Gly Ser Gly Lys Gly Glu Leu Phe Leu Val Ala Val Ser Ala Ile			
445	450	455	
gcc gaa aag ctc cgc cag gcc aag cag agt tcg tcc gcg gcg ctc agc			1504
Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser Ser Ala Ala Leu Ser			
460	465	470	
aag ttt atc gcc gtc tac ttt gat tat tcc tgc gag gga gac gtc ccc			1552
Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro			
475	480	485	
ggt atc cta gac ctg agt acc aag tac aga ctc atg gac aat ctt cct			1600
Gly Ile Leu Asp Leu Ser Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro			
490	495	500	505
cag ctc tgt tcc cac ttg cac tcc cga gac cac ggc ctc cag gag ccg			1648
Gln Leu Cys Ser His Leu His Ser Arg Asp His Gly Leu Gln Glu Pro			
510	515	520	
ggg cag cac acg cga cag ggc agc aga agg aac tac ttc cgg agc aag			1696
Gly Gln His Thr Arg Gln Gly Ser Arg Arg Asn Tyr Phe Arg Ser Lys			
525	530	535	
tca ggc cgg tcc cta tac gtc gcc att tgc aac atg cac cag ttt att			1744
Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His Gln Phe Ile			
540	545	550	
gac gag gag ccc gac tgg ttc gaa aag cag ttc gtt ccc ttc cat cct			1792
Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Val Pro Phe His Pro			
555	560	565	
cct cca ctg cgc tac cgg gag cca gtc ttg gag aaa ttt gat tcg ggc			1840
Pro Pro Leu Arg Tyr Arg Glu Pro Val Leu Glu Lys Phe Asp Ser Gly			
570	575	580	585

ttg gtt tta aat gat gtc atg tgc aaa cca ggg cct gag agt gac ttc			1888
Leu Val Leu Asn Asp Val Met Cys Lys Pro Gly Pro Glu Ser Asp Phe			
590	595	600	
tgc cta aag gta gag gcg gct gtt ctt ggg gca acc gga cca gcc gac			1936
Cys Leu Lys Val Glu Ala Ala Val Leu Gly Ala Thr Gly Pro Ala Asp			
605	610	615	
tcc cag cac gag agt cag cat ggg ggc ctg gac caa gac ggg gag gcc			1984
Ser Gln His Glu Ser Gln His Gly Gly Leu Asp Gln Asp Gly Glu Ala			
620	625	630	
cg ^g cct gcc ctt gac ggt agc gcc gcc ctg caa ccc ctg ctg cac acg			2032
Arg Pro Ala Leu Asp Gly Ser Ala Ala Leu Gln Pro Leu Leu His Thr			
635	640	645	
gtg aaa gcc ggc agc ccc tcg gac atg ccg ccg gac tca ggc atc tat			2080
Val Lys Ala Gly Ser Pro Ser Asp Met Pro Arg Asp Ser Gly Ile Tyr			
650	655	660	665
gac tcg tct gtg ccc tca tcc gag ctg tct ctg cca ctg atg gaa gga			2128
Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu Pro Leu Met Glu Gly			
670	675	680	
ctc tcg acg gac cag aca gaa acg tct tcc ctg acg gag agc gtg tcc			2176
Leu Ser Thr Asp Gln Thr Glu Thr Ser Ser Leu Thr Glu Ser Val Ser			
685	690	695	
tcc tct tca ggc ctg ggt gag gag gaa cct cct gcc ctt cct tcc aag			2224
Ser Ser Ser Gly Leu Gly Glu Glu Pro Pro Ala Leu Pro Ser Lys			
700	705	710	
ctc ctc tct tct ggg tca tgc aaa gca gat ctt ggt tgc cgc agc tac			2272
Leu Leu Ser Ser Gly Ser Cys Lys Ala Asp Leu Gly Cys Arg Ser Tyr			
715	720	725	
act gat gaa ctc cac gcg gtc gcc cct ttg taacaaaacg aaagagtcta			2322
Thr Asp Glu Leu His Ala Val Ala Pro Leu			
730	735		
agcattgccatcttagctg			2341

<210> 8
 <211> 739
 <212> PRT
 <213> Homo sapiens

<400> 8
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 35 40 45
 Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
 50 55 60
 Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
 65 70 75 80
 Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
 85 90 95
 Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
 100 105 110
 Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln Leu
 115 120 125
 Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Lys Arg Thr Gly
 130 135 140
 Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
 145 150 155 160
 Val Lys Val Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His
 165 170 175
 Pro Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp
 180 185 190
 Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser
 195 200 205
 Gln His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn
 210 215 220
 Phe Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly
 225 230 235 240
 Pro Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Thr Thr
 245 250 255
 Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu
 260 265 270
 Val Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys
 275 280 285

Pro Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr
 290 295 300
 Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met
 305 310 315 320
 Cys Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu
 325 330 335
 Ser Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu
 340 345 350
 Arg Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln
 355 360 365
 Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe
 370 375 380
 Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys
 385 390 395 400
 Arg Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln
 405 410 415
 Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys
 420 425 430
 Lys Asn Tyr Lys His Lys Gly Gly Arg Gly Ser Gly Lys Gly Glu
 435 440 445
 Leu Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala
 450 455 460
 Lys Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe
 465 470 475 480
 Asp Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr
 485 490 495
 Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His
 500 505 510
 Ser Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly
 515 520 525
 Ser Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val
 530 535 540
 Ala Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe
 545 550 555 560
 Glu Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu
 565 570 575
 Pro Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met
 580 585 590
 Cys Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala
 595 600 605
 Val Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His
 610 615 620

Gly Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser
 625 630 635 640
 Ala Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser
 645 650 655
 Asp Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser
 660 665 670
 Glu Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu
 675 680 685
 Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu
 690 695 700
 Glu Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys
 705 710 715 720
 Lys Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val
 725 730 735
 Ala Pro Leu

<210> 9

<211> 2217

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate nucleotide sequence encodes the amino acid sequence of SEQ ID NO:8.

<221> misc_feature

<222> (1)...(2217)

<223> n = A,T,C or G

<400> 9

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tggmnggng	tnggncncngc	nwsnmgnaaay	wsnggnytnt	ayaayathac	nttyaartay	180
gayaaytgya	cnacontayyt	naayccngtn	ggnnaarcayg	tnathgcnga	ygcncaaraay	240
athacnathw	sncartaygc	ntgycaygay	cargtngcng	tnacnathyt	ntggwsncn	300
ggngcnytng	gnathgartt	yytnaarggn	ttymgngtna	thytnrgarga	rytnaarwsn	360
garggnmgnc	artgycarca	rytnathytn	aargayccna	arcarytnaa	ywsnwsntty	420
aarmgnacng	gnatggarws	ncarcntty	yttnaayatga	arttygarac	ngaytaytty	480
gttnaargtng	tnccnttycc	nwsnathaar	aaygarwsna	aytaycaycc	nttytaytty	540
mgnacnmng	cntgygayyt	nytnytnca	ccngayaayy	tngcntgyaa	rccnttgytgg	600
aarccnmgn	ayytnaayat	hwsncarcay	ggnwsngaya	tgcargtnws	nttygaycay	660
gcnccncaya	aytayggntt	ymgnatty	tayytncayt	ayaarytnaa	rcaygarggn	720
ccnttyaarm	gnaaracntg	yaarcargar	caracnacng	aracnacnws	ntgyytnytn	780

caraaygtnw	snccnggnga	ytayathath	garytngtng	aygayacnaa	iacnacnmgn	840
aargtnatgc	aytaygcnyt	naarccngtn	caywsncnt	ggcnggncc	nathmgnngcn	900
gtngcnatha	cngtnccnyt	ngtngtnath	wsngcnttyg	cnacnytntt	iacngtnatg	960
tgymgnaara	arcarcarga	raayathtay	wsncayyng	aygargarws	nwsngarwsn	1020
wsnacntaya	cngcngcnyt	nccnmngar	mgnymngnc	cnmgnccnaa	rgtnttynytn	1080
tgytaywsnw	snaargaygg	ncaraaycay	atgaaygtng	tncartgytt	ycntaytty	1140
ytnccargayt	tytgyggntg	ygargtngcn	ytngaytnt	gggargaytt	ywsnytnntgy	1200
mngarggnc	armngngartg	ggttnathcar	aarathcayg	arwsncartt	yathathgtn	1260
gtntgywsna	arggnatgaa	rtayttygtn	gayaaraara	aytayaarca	yaarggnggn	1320
ggnmnggnw	sngnaargg	ngarytnnty	ytngtngcng	tnwsngcnat	hgcngraraar	1380
ytnmgnrcarg	cnaarcarws	nwsnwsgcn	gcnytnwsna	arttyathgc	ngtntaytty	1440
gaytaywsnt	gygarggng	ygtncnggn	athytngayy	tnwsnacnaa	rtaymgnyn	1500
atggayaayy	tnccncaryt	ntgywsncay	ytnccaywsnm	gngaycaygg	nytnccargar	1560
ccnggnarc	ayacnmgnca	rggnwsnmgn	mgnaytayt	tymgnwsnaa	rwsnggnmgn	1620
wsnytnayg	tngcnathtg	yaayatgcay	carttyathg	aygargarcc	ngaytggty	1680
garaarcart	tygtncntt	ycayccnccn	ccnytnmgnt	aymngarcc	ngtnytngrar	1740
aarttygayw	sngnytngt	nytnaaygay	gtnatgtgya	arccngncc	ngarwsngay	1800
ttytgyytna	argtngargc	ngcngtnytn	gngcnacng	gnccngcng	ywsncarcay	1860
garwsncarc	ayggnggnyt	ngaycargay	gngargcnm	gnccngcnyt	ngayggwnsn	1920
gngnytnwsna	cngaycarac	ngaracnwsn	wsnytnacng	arwsngtnws	nwsnwsnwsn	1980
gngnytnngng	argargarcc	nccngcnyt	ccnwsnaary	tnytnwsnws	nggnwsntgy	2040
aargcngayy	tngntgymg	nwsntayacn	gaygarytnc	aygcngrng	nccnyt	2100
						2160
						2217

<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide linker.

<400> 10

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<210> 11

<211> 2443

<212> DNA

<213> Mouse

<220>

<221> CDS
 <222> (101)...(2317)

<400> 11

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				Met	Ala	Pro	Trp	Leu								
				1				5								
cag	ctc	tgc	tcc	ttc	ttc	act	gtc	aac	gcc	tgt	ctc	aac	ggc	tcg	163	
Gln																
Leu	Cys	Ser	Phe	Phe	Phe	Thr	Val	Asn	Ala	Cys	Leu	Asn	Gly	Ser		
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cag	ctg	gca	gtg	gcc	gcf	ggc	tcc	ggc	cgc	gcf	agg	ggc	gcf	gac	211	
Gln																
Leu	Ala	Val	Ala	Ala	Gly	Gly	Ser	Gly	Arg	Ala	Arg	Gly	Ala	Asp		
25															35	
acc	tgt	ggc	tgg	agg	gga	gtg	ggg	ccg	gcc	agc	agg	aac	agc	gga	ctg	259
Thr	Cys	Gly	Trp	Arg	Gly	Val	Gly	Pro	Ala	Ser	Arg	Asn	Ser	Gly	Leu	
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cac	aac	atc	acc	ttc	aga	tac	gac	aac	tgt	acc	acc	acc	acc	acc	ccc	307
His	Asn	Ile	Thr	Phe	Arg	Tyr	Asp	Asn	Cys	Thr	Thr	Tyr	Leu	Asn	Pro	
55															65	
ggc	ggc	ggg	aag	cat	gcf	att	gct	gat	gct	cag	aac	atc	acc	atc	agc	355
Gly	Gly	Gly	Lys	His	Ala	Ile	Ala	Asp	Ala	Gln	Asn	Ile	Thr	Ile	Ser	
70															85	
cag	tac	gct	cac	gac	cag	gtg	gca	gtc	acc	att	ctt	tgg	tcc	cca	403	
Gln	Tyr	Ala	Cys	His	Asp	Gln	Val	Ala	Val	Thr	Ile	Leu	Trp	Ser	Pro	
90															100	
ggg	gcc	ctt	ggc	att	gaa	ttc	cta	aaa	gga	ttc	cga	gtc	atc	ctg	gag	451
Gly	Ala	Leu	Gly	Ile	Glu	Phe	Leu	Lys	Gly	Phe	Arg	Val	Ile	Leu	Glu	
105															115	
gag	ctg	aag	tgc	gag	ggc	aga	cag	tgc	caa	cag	ctg	att	cta	aag	gac	499
Glu	Leu	Lys	Ser	Glu	Gly	Arg	Gln	Cys	Gln	Gln	Leu	Ile	Leu	Lys	Asp	
120															130	
ccc	aaa	cag	ctc	aac	agc	agc	ttc	aga	agg	act	gga	atg	gaa	tct	cag	547

Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr Gly Met Glu Ser Gln			
135	140	145	
cct ttc ctg aat atg aaa ttt gag acg gat tac ttt gta aag att gtc			595
Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe Val Lys Ile Val			
150	155	160	165
cct ttc cct tcc att aaa aat gaa agc aat tac cat ccc ttc ttc ttc			643
Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr His Pro Phe Phe Phe			
170	175	180	
aga aca cg ^g gcc tgt gac ctg ttg tta caa cct gac aac ttg gcc tgt			691
Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn Leu Ala Cys			
185	190	195	
aag cct ttc tgg aag cct cga aac ctg aat atc agc cag cat ggt tct			739
Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln His Gly Ser			
200	205	210	
gac atg cac gt ^g tcc ttc gac cat gcc ccg cag aac ttc ggc ttc cgt			787
Asp Met His Val Ser Phe Asp His Ala Pro Gln Asn Phe Gly Phe Arg			
215	220	225	
ggc ttc cat gtt ctc tat aag ctc aag cac gaa ggc ccc ttc agg ccg			835
Gly Phe His Val Leu Tyr Lys Leu Lys His Glu Gly Pro Phe Arg Arg			
230	235	240	245
agg act tgc agg cag gac cag aat aca gag aca acc agc tgc ctc ctc			883
Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr Thr Ser Cys Leu Leu			
250	255	260	
caa aac gtt tct cca ggg gac tat atc att gag ctg gt ^g gat gac agc			931
Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val Asp Asp Ser			
265	270	275	
aac acc acc agg aaa gct gct cag tat gt ^g gt ^g aag tca gt ^g cag tct			979
Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val Lys Ser Val Gln Ser			
280	285	290	
ccc tgg gct gga ccc atc aga gct gt ^g gcc atc act gt ^g cct ctg gtt			1027
Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val Pro Leu Val			
295	300	305	

gtc ata tct gcg ttc gca acc ctg ttc act gtg atg tgc aga aag aag			1075
Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys Arg Lys Lys			
310	315	320	325
caa caa gaa aat ata tat tca cat tta gat gaa gaa agc ccg gag tcg			1123
Gln Gln Asn Ile Tyr Ser His Leu Asp Glu Glu Ser Pro Glu Ser			
330	335	340	
tcc aca tac gct gcg gct ctc ccc aga gac agg ctc ccg cct cag ccc			1171
Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg Leu Arg Pro Gln Pro			
345	350	355	
aag gtc ttc ctc tgc tac tcc aat aaa gat ggc cag aat cac atg aac			1219
Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly Gln Asn His Met Asn			
360	365	370	
gtg gtc cag tgt ttc gcc tat ttc ctg caa gat ttc tgt ggc tgt gag			1267
Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys Gly Cys Glu			
375	380	385	
gtg gct ctg gac ttg tgg gaa gat ttc agc ctc tgc aga gag ggg cag			1315
Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg Glu Gly Gln			
390	395	400	405
aga gaa tgg gcc att cag aag atc cac gag tcc cag ttc atc att gtc			1363
Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser Gln Phe Ile Ile Val			
410	415	420	
gtg tgc tcc aaa ggc atg aag tac ttt gta gat aag aag aac ttc aga			1411
Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys Asn Phe Arg			
425	430	435	
cac aaa gga ggc agc cgc ggc gag gcg caa ggc gag ttc ttc ctg gtg			1459
His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly Glu Phe Phe Leu Val			
440	445	450	
gcc gtg gca gcc att gct gag aag ctc cgt cag gcc aag cag agc tca			1507
Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys Gln Ser Ser			
455	460	465	
tct gcc gca ctg cgc aag ttc atc gcc gtc tac ttc gat tat tcc tgt			1555

Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr Phe Asp Tyr Ser Cys			
470	475	480	485
gaa ggg gat gta ccc tgc agc ctg gac ctg agc acc aag tac aag ctc			1603
Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser Thr Lys Tyr Lys Leu			
490	495	500	
atg gac cac ctt cct gag ctc tgt gcc cat ctg cac tca gga gag cag			1651
Met Asp His Leu Pro Glu Leu Cys Ala His Leu His Ser Gly Glu Gln			
505	510	515	
gag gtg ctg ggt cag cac cca ggc cac agc agc aga agg aac tac ttc			1699
Glu Val Leu Gly Gln His Pro Gly His Ser Ser Arg Arg Asn Tyr Phe			
520	525	530	
cgg agc aaa tcg ggc cgc tcc ctg tat gtt gcc att tgc aac atg cac			1747
Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala Ile Cys Asn Met His			
535	540	545	
cag ttt att gat gag gag cct gac tgg ttt gag aag cag ttt ata ccc			1795
Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu Lys Gln Phe Ile Pro			
550	555	560	565
ttc caa cat ccc cct gtg cgc tac cag gag cca gtc ctg gag aaa ttt			1843
Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro Val Leu Glu Lys Phe			
570	575	580	
gac tca ggc ttg gtt tta aat gat gtc ata agc aaa cca ggg cca gag			1891
Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser Lys Pro Gly Pro Glu			
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agt gac ttc tgt cgg aaa gtc gag gct tgt gta ctt ggg gcc gct ggg			1939
Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val Leu Gly Ala Ala Gly			
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cca gcc gac tct tat tca tac ctg gag agt cag cat gta ggc ctg gac			1987
Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln His Val Gly Leu Asp			
615	620	625	
caa gac act gag gcc cag ccc tcc tgt gat agt gcc cct gcc ttg cag			2035
Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser Ala Pro Ala Leu Gln			
630	635	640	645

ccc ctg tta cac gca gtg aaa gct ggc agt ccc tca gag atg cca cg	650	655	660	2083
Pro Leu Leu His Ala Val Lys Ala Gly Ser Pro Ser Glu Met Pro Arg				
gac tca ggc ata tat gat tct tct gta ccc tca tca gag ctc tct ctg	665	670	675	2131
Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu Leu Ser Leu				
cct ctg atg gag gga ctc tcc ccg gat cag ata gaa aca tct tct ctg	680	685	690	2179
Pro Leu Met Glu Gly Leu Ser Pro Asp Gln Ile Glu Thr Ser Ser Leu				
acc gag agt gta tct tcc tcc tct ggc cta ggt gag gag gac ccc cct	695	700	705	2227
Thr Glu Ser Val Ser Ser Ser Gly Leu Gly Glu Glu Asp Pro Pro				
acc ctc cct tcc aag ctc ttt gcc tct ggg gtg tcc aga gaa cat ggt	710	715	720	2275
Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val Ser Arg Glu His Gly				
tgc cac agc cac act gac gaa ctg caa gcg ctt gct cct ttg	730	735		2317
Cys His Ser His Thr Asp Glu Leu Gln Ala Leu Ala Pro Leu				
taaggactcg gaagagtcta agcatcgcca cttagctgc tgatctctct ggctccccag				2377
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Ala Arg Gly Ala Asp Thr Cys Gly Trp Arg Gly Val Gly Pro Ala Ser	35	40	45	
Arg Asn Ser Gly Leu His Asn Ile Thr Phe Arg Tyr Asp Asn Cys Thr	50	55	60	

Thr Tyr Leu Asn Pro Gly Gly Lys His Ala Ile Ala Asp Ala Gln
 65 70 75 80
 Asn Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr
 85 90 95
 Ile Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe
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 Arg Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Cys Gln Gln
 115 120 125
 Leu Ile Leu Lys Asp Pro Lys Gln Leu Asn Ser Ser Phe Arg Arg Thr
 130 135 140
 Gly Met Glu Ser Gln Pro Phe Leu Asn Met Lys Phe Glu Thr Asp Tyr
 145 150 155 160
 Phe Val Lys Ile Val Pro Phe Pro Ser Ile Lys Asn Glu Ser Asn Tyr
 165 170 175
 His Pro Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Gln Pro
 180 185 190
 Asp Asn Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile
 195 200 205
 Ser Gln His Gly Ser Asp Met His Val Ser Phe Asp His Ala Pro Gln
 210 215 220
 Asn Phe Gly Phe Arg Gly Phe His Val Leu Tyr Lys Leu Lys His Glu
 225 230 235 240
 Gly Pro Phe Arg Arg Arg Thr Cys Arg Gln Asp Gln Asn Thr Glu Thr
 245 250 255
 Thr Ser Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu
 260 265 270
 Leu Val Asp Asp Ser Asn Thr Thr Arg Lys Ala Ala Gln Tyr Val Val
 275 280 285
 Lys Ser Val Gln Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile
 290 295 300
 Thr Val Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val
 305 310 315 320
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 325 330 335
 Glu Ser Pro Glu Ser Ser Thr Tyr Ala Ala Ala Leu Pro Arg Asp Arg
 340 345 350
 Leu Arg Pro Gln Pro Lys Val Phe Leu Cys Tyr Ser Asn Lys Asp Gly
 355 360 365
 Gln Asn His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp
 370 375 380
 Phe Cys Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu
 385 390 395 400

Cys Arg Glu Gly Gln Arg Glu Trp Ala Ile Gln Lys Ile His Glu Ser
 405 410 415
 Gln Phe Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp
 420 425 430
 Lys Lys Asn Phe Arg His Lys Gly Gly Ser Arg Gly Glu Ala Gln Gly
 435 440 445
 Glu Phe Phe Leu Val Ala Val Ala Ala Ile Ala Glu Lys Leu Arg Gln
 450 455 460
 Ala Lys Gln Ser Ser Ala Ala Leu Arg Lys Phe Ile Ala Val Tyr
 465 470 475 480
 Phe Asp Tyr Ser Cys Glu Gly Asp Val Pro Cys Ser Leu Asp Leu Ser
 485 490 495
 Thr Lys Tyr Lys Leu Met Asp His Leu Pro Glu Leu Cys Ala His Leu
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 His Ser Gly Glu Gln Glu Val Leu Gly Gln His Pro Gly His Ser Ser
 515 520 525
 Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
 530 535 540
 Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
 545 550 555 560
 Lys Gln Phe Ile Pro Phe Gln His Pro Pro Val Arg Tyr Gln Glu Pro
 565 570 575
 Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Ile Ser
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 Lys Pro Gly Pro Glu Ser Asp Phe Cys Arg Lys Val Glu Ala Cys Val
 595 600 605
 Leu Gly Ala Ala Gly Pro Ala Asp Ser Tyr Ser Tyr Leu Glu Ser Gln
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 His Val Gly Leu Asp Gln Asp Thr Glu Ala Gln Pro Ser Cys Asp Ser
 625 630 635 640
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 645 650 655
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 660 665 670
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 675 680 685
 Glu Thr Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Gly Leu Gly
 690 695 700
 Glu Glu Asp Pro Pro Thr Leu Pro Ser Lys Leu Phe Ala Ser Gly Val
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Ala Pro Leu

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<211> 2217

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<213> Artificial Sequence

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<221> misc_feature

<222> (1)...(2217)

<223> n = A, T, C or G

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